

FEATURES	source	Location/Qualifiers
		1. 1.2232
		/organism="unknown"
BASE COUNT	602 a	464 c 508 g 658 t
ORIGIN		
Query Match		Score 2232; DB 6; Length 2232;
Best Local Similarity	100.0%	Score 2232; DB 6; Length 2232;
Matches 2232;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1 GGATGAAACAGGGCATTCGCCAGTACATCCACAAATGCTGTCACATCTCGTCT 60	
Db	1 GGATGAAACAGGGCATTCGCCAGTACATCCACAAATGCTGTCACATCTCGTCT 60	
Qy	61 CGGTTATCGAAATACCAACGAGAGTCAACCCCTTGTATTGAT 120	
Db	61 CGGTTATCGAAATACCAACGAGAGTCAACCCCTTGTATTGAT 120	
Qy	121 TACGGTGCCTCTGTCATAAATTGACGTGAAAGCAATTGGGCCAACCTCCTGC 180	
Db	121 TACGGTGCCTCTGTCATAAATTGACGTGAAAGCAATTGGGCCAACCTCCTGC 180	
Qy	181 CTCFACTCCTGGTTCATCTTGGTTCATCTTGGCAAAATGCTGTCATCTA 240	
Db	181 CTCFACTCCTGGTTCATCTTGGCAAAATGCTGTCATCTA 240	
Qy	241 ATAAACTGAAAAGCTGAAAGTGTGACTTGACATTACTGTCAACCTGGCCATCT 300	
Db	241 ATAAACTGAAAAGCTGAAAGTGTGACTTGACATTACTGTCAACCTGGCCATCT 300	
Qy	301 GATCTGCTTTTCATTAATPACTCCCATGGGCTCACTCTGTGCAAAATGAGTGGTC 360	
Db	301 GATCTGCTTTTCATTAATPACTCCCATGGGCTCACTCTGTGCAAAATGAGTGGTC 360	
Qy	361 TTGGGAATGCAATTATTACAGGGGTGATACATCGTTATTGGCGGA 420	
Db	361 TTGGGAATGCAATTATTACAGGGGTGATACATCGTTATTGGCGGA 420	
Qy	421 ATCTCTCATCATCCCTGCAATCGTCAAGGCTGTATCACATCGTCAATGACTGGTC 480	
Db	421 ATCTCTCATCATCCCTGCAATCGTCAAGGCTGTATCACATCGTCAATGACTGGTC 480	
Qy	481 GCTTAAAGCCAGGACGGTCACCTTGGGTGGTACAAGCTGTATCACCTGGTGTG 540	
Db	481 GCTTAAAGCCAGGACGGTCACCTTGGGTGGTACAAGCTGTATCACCTGGTGTG 540	
Qy	541 GCTGTTGGCCTTACTTCACAGGAGGAAATTCACATCGTCAATGAGAAC 600	
Db	541 GCTGTTGGCCTTACTTCACAGGAGGAAATTCACATCGTCAATGAGAAC 600	
Qy	601 TATGTCCTGTCGCCCTTATTCACAGGAGGAAATTCACATCGTCAATGAGAAC 660	
Db	601 TATGTCCTGTCGCCCTTATTCACAGGAGGAAATTCACATCGTCAATGAGAAC 660	
Qy	661 ATTTGGCTTGGCTTACTTCACAGGAGGAAATTCACATCGTCAATGAGAAC 720	
Db	661 ATTTGGCTTGGCTTACTTCACAGGAGGAAATTCACATCGTCAATGAGAAC 720	
Qy	721 ACCCTGCTTGGCTTACTTCACAGGAGGAAATTCACATCGTCAATGAGAAC 780	
Db	721 ACCCTGCTTGGCTTACTTCACAGGAGGAAATTCACATCGTCAATGAGAAC 780	
Qy	781 ATCATGATGTTACTTCACAGGAGGAAATTCACATCGTCAATGAGAAC 840	
Db	781 ATCATGATGTTACTTCACAGGAGGAAATTCACATCGTCAATGAGAAC 840	
Qy	841 TTCCAGGAATCTCGGGCTTGTACTGAAACCCAGTCACTGGAAATCCGTGAA 900	
Db	841 TTCCAGGAATCTCGGGCTTGTACTGAAACCCAGTCACTGGAAATCCGTGAA 900	
Qy	901 CAGGTGACAGACTCTGGATGACTCTGGCAACTTGGAAACTAGCTGGACTATGGC 2040	
Db	901 CAGGTGACAGACTCTGGATGACTCTGGCAACTTGGAAACTAGCTGGACTATGGC 2040	

Qy	2041	TCTACTTTCAGGCCACATGGCTTAAGAAGCTTTCAGAAAGAACTGGGACAGAGCAAC	2100
Qy	2041	TCTACTTTCAGGCCACATGGCTTAAGAAGCTTTCAGAAAGAACTGGGACAGAGCAAC	2100
Qy	2101	TTCACCCCTCATATTCGTATGTCCTATGAAATGCTAAATGTTAAGTGTATGGTA	2160
Qy	2101	TTCACCCCTCATATTCGTATGTCCTATGAAATGCTAAATGTTAAGTGTATGGTA	2160
Qy	2161	TGAATGTAATAACTGTTAACACTATGTTGAAATAATCAATGCTATACTAACTA	2220
Qy	2161	TGAATGTAATAACTGTTAACACTATGTTGAAATAATCAATGCTATACTAACTA	2220
Db	2161	TGAATGTAATAACTGTTAACACTATGTTGAAATAATCAATGCTATACTAACTA	2220
RESULT	2		
LOCUS	179542	179542	2232 bp
DEFINITION		Sequence 1 from patent US 5707815.	
ACCESSION	I79542		
VERSION	I79542.1	GI:3207832	
KEYWORDS			
SOURCE		Unknown.	
ORGANISM		Unclassified.	
REFERENCE	1	(bases 1 to 2232)	
AUTHORS	Charo, I.F. and Coughlin, S.R.		
TITLE	Mammalian monocyte chemoattractant protein receptors and assays		
using them			
JOURNAL	Patent: US 5707815-A	13-JAN-1998;	
FEATURES	Patent	Location/Qualifiers	
source	1..2232	/organism="unknown"	
BASE COUNT	602	a 464 c 508 g 658 t	
ORIGIN			
Query Match	100.0%	Score 2232; DB 6; Length 2232;	
Best Local Similarity	100.0%	Pred. No: 0;	
Matches 2232;	Conservative 0;	Mismatches 0;	
		Indels 0;	
		Gaps 0	
Qy	1	GGATTGACAAAGGCAATTTCGCCAGTACATGCCACACAGATGGCTGCCACATCGTGTCT	60
Db	1	GGATTGACAAAGGCAATTTCGCCAGTACATGCCACACAGCTGCCACATCGTGTCT	60
Qy	61	CGTTTATCAGAAATACCAACGAGGCGGTGAAAGTACCACTTTTGATATGAT	120
Db	61	CGTTTATCAGAAATACCAACGAGGCGGTGAAAGTACCACTTTTGATATGAT	120
Qy	121	TACGGTGTCCCTGTCATAATTGACGTGAAGCAATTGGGCCAACCTGCTGCTCG	180
Db	121	TACGGTGTCCCTGTCATAATTGACGTGAAGCAATTGGGCCAACCTGCTGCTCG	180
Qy	181	CCTACTGCCTGGTTGTCATCTTGGTTGTCATGCTGTCATCTCATCTA	240
Db	181	CCTACTGCCTGGTTGTCATCTTGGTTGTCATGCTGTCATCTCATCTA	240
Qy	241	ATAAACTGGAAAGCTGAAGTGTGACTGACATTACCTGCTCAACCTGGCCATCT	300
Db	241	ATAAACTGGAAAGCTGAAGTGTGACTGACATTACCTGCTCAACCTGGCCATCT	300
Qy	301	GATCTGCTTTCTCTTATTAATCTCCATGTCATGATAGATCTGGCTCATCTGCT	480
Db	301	GATCTGCTTTCTCTTATTAATCTCCATGTCATGATAGATCTGGCTCATCTGCT	480
Qy	361	TTTGGGAATGCAATTGCAAAATTATTCACACGGCTATCACATCGTTATTTGGCGA	420
Db	361	TTTGGGAATGCAATTGCAAAATTATTCACACGGCTATCACATCGTTATTTGGCGA	420
Qy	421	ATCTCTTCATCATCTCCGACAACTGGCTTATGTCATGCTGTT	480
Db	421	ATCTCTTCATCATCTCCGACAACTGGCTTATGTCATGCTGTT	480

4.81	QY	541	GCTTTAAAGCCAGGACGGTCACCTTGGGTGGTGGACAGTGTGATCAGCTGGTTGGTGTG	540
4.81	Db	541	GCTGTGTTGCTGCTGCCAGGATCATCTTAAATGCCAGAAGAGATTCCTG	540
QY	541	GCTGTGTTGCTGCTGCCAGGATCATCTTAAATGCCAGAAGAGATTCCTG	540	
Db	541	GCTGTGTTGCTGCTGCCAGGATCATCTTAAATGCCAGAAGAGATTCCTG	540	
QY	601	TATGTCGTGGCCTTATTCCAGAGATGGATAATTCCACACAATAATGGAAAC	660	
Db	601	TATGTCGTGGCCTTATTCCAGAGATGGATAATTCCACACAATAATGGAAAC	660	
QY	661	ATTTGGGGCTGCTGGCTCATGGCATCTGGCTACTCGGATCTCTGAA	720	
Db	661	ATTTGGGGCTGCTGGCTCATGGCATCTGGCTACTCGGATCTCTGAA	720	
QY	721	ACCCGTGTTGCGTGTGAAAAGCAGAAAGGGCATAGGGATAAGGGATAAGG	780	
Db	721	ACCCGTGTTGCGTGTGAAAAGCAGAAAGGGCATAGGGATAAGGAGTGGAGT	780	
QY	781	ATCATGATTGTTACTTCTCTGACTCTGACTCTGACTCTGACTCTG	840	
Db	781	ATCATGATTGTTACTTCTCTGACTCTGACTCTGACTCTGACTCTG	840	
QY	841	TTCAGGAATTCTGCGCTGAGTACTGTGAAAGGACCGTCACTTGACAA	900	
Db	841	TTCAGGAATTCTGCGCTGAGTACTGTGAAAGGACCGTCACTTGACAA	900	
QY	901	CAGGTACAGAACGACTCTGGATGACTCACTGTGCTGATCACTCCAT	960	
Db	901	CAGGTACAGAACGACTCTGGATGACTCACTGTGCTGATCACTCCAT	960	
QY	961	GTTGGGAGAGTCAAGGCCTTTTCACATAGCTTGGCTGTAAGGATTGCCAC	1020	
Db	961	GTTGGGAGAGTCAAGGCCTTTTCACATAGCTTGGCTGTAAGGATTGCCAC	1020	
QY	1021	CAAAACCAGTGTGAGGTCAGGAGTGGACCAAGAAAGATGCAAAAGTCA	1080	
Db	1021	CAAAACCAGTGTGAGGTCAGGAGTGGACCAAGAAAGATGCAAAAGTCA	1080	
QY	1081	CAAGGACTCTCGATGTCGTTGAAAGGAAGTCAATTGGCAAGGCCCTGT	1140	
Db	1081	CAAGGACTCTCGATGTCGTTGAAAGGAAGTCAATTGGCAAGGCCCTGT	1140	
QY	1141	CTTCAGCAAAAGAAGGAGCTAGAGCTTGAAGACAGATACTCTGCTTGGAA	1200	
Db	1141	CTTCAGCAAAAGAAGGAGCTAGAGCTTGAAGACAGATACTCTGCTTGGAA	1200	
QY	1201	CGTCCTGCTTCAAGAGTGTGATTCAGTGTGATCTGGGCTCTAGTTAC	1260	
Db	1201	CGTCCTGCTTCAAGAGTGTGATTCAGTGTGATCTGGGCTCTAGTTAC	1260	
QY	1261	GGAAGGCTGAGGGAGAGACTCCAGTGGTTGAAAGCATTTTCAACTAC	1320	
Db	1261	GGAAGGCTGAGGGAGAGACTCCAGTGGTTGAAAGCATTTTCAACTAC	1320	
QY	1321	TCCAGTTCCTCATTTGAATACAGGCTAGACTTTCAAGCTTTTAATAGT	1380	
Db	1321	TCCAGTTCCTCATTTGAATACAGGCTAGACTTTCAAGCTTTTAATAGT	1380	
QY	1381	AAATTAAGCTGAAATGCAACTGTAAATGGTAAGAGTTAGTTGAGTCT	1440	
Db	1381	AAATTAAGCTGAAATGCAACTGTAAATGGTAAGAGTTAGTTGAGTCT	1440	
QY	1441	CATGTCAAACGTCGAAATGCTGTATAGTCAGACTTGTGAGCTTGA	150	
Db	1441	CATGTCAAACGTCGAAATGCTGTATAGTCAGACTTGTGAGCTTGA	150	
QY	1501	ATTTGAGCAGGTGGTATGTTGGAGACTGCTGATCAACCCAAATAGT	156	
Db	1501	ATTTGAGCAGGTGGTATGTTGGAGACTGCTGATCAACCCAAATAGT	156	

Qy	1561	AGGAGTTGGAAAGTGTGTGATCTGTGGCACATTAGCCTATGTGCAGCATCTAAGTA	1620	JOURNAL	Submitted (01-DEC-1993)	Scott J. Myers, Cardiovascular, The Gladstone Institutes, 2550 23rd street, San Francisco, CA 94110.
Db	1561	AGGAGTTGGAAAGTGTGTGATCTGTGGCACATTAGCCTATGTGCAGCATCTAAGTA	1620	FEATURES	Location/Qualifiers	
Qy	1621	ATGATGTCCTTTGAAATCACAGTATACGCCATCAGTCATCTGCATCTGCATCTGCAT	1680	source	1. .2232	"Homo sapiens"
Db	1621	ATGATGTCCTTTGAAATCACAGTATACGCCATCAGTCATCTGCATCTGCATCTGCAT	1680		/db_xref="taxon:9606"	
Qy	1681	CTCTCAGGGTTGTGCCAAGGCCTTTGTGTATATTGAACTCATGC	1740		/clone="CCR2-9a"	
Db	1681	CTCTCAGGGTTGTGCCAAGGCCTTTGTGTATATTGAACTCATGC	1740		/cell_line="Monocytic 6"	
Qy	1741	GTTTAATCACATTCGAGTTTCAGTGTCTGCAGATGTCTGATGCATATGTGCC	1800		/clone_lib="Monocytic 4"	
Db	1741	GTTTAATCACATTCGAGTTTCAGTGTCTGCAGATGTCTGATGCATATGTGCC	1800		/standard_name="monocyte chemoattractant protein 1 receptor"	
Qy	1801	CTAATTTGCCAGTGTGAACTCCCTAAATCAAAATGCTTTAACCT	1860		/note="alternatively spliced; MCP-1RA"	
Db	1801	CTAATTTGCCAGTGTGAACTCCCTAAATCAAAATGCTTTAACCT	1860		/codon_start=1	
Qy	1861	ATGGTAAAGAATGGAAAGTGGAGAACGCTCCCTGAAAGAACACTTCCCTCTA	1920		/product="MCP-1 receptor"	
Db	1861	ATGGTAAAGAATGGAAAGTGGAGAACGCTCCCTGAAAGAACACTTCCCTCTA	1920		/protein_id="AAAI9119_1"	
Qy	1921	CGAGGCCAAGTTAAGAACATCTCTATGTGCCAGTGTCTGATGCAGCAG	1980		/db_xref="GT:7256"	
Db	1921	CGAGGCCAAGTTAAGAACATCTCTATGTGCCAGTGTCTGATGCAGCAG	1980		/translation="MUS1RSR1RNTNESGEVTEDYDYGAPCHKFDVKIGAQI	
Qy	1981	AAACACTGGCTCTAGACCAAGGAACACTGGAAACTGCCAAACTGGACTATGCC	2040		LPPLYSLVTFYFGNMVNLVILNCCKLKCLTDIYLNLATSDLLFLITLPLWAHSA	
Db	1981	AAACACTGGCTCTAGACCAAGGAACACTGGAAACTGCCAAACTGGACTATGCC	2040		ANENYGNANCKLFTGLYHIGKIFLILIDRYLIAVHFAVFLKARTYFGVVT	
Qy	2041	TCTACCTTCAGGCCATCTGGTAAGAGTGGCCAGTGTCTGATGCCAAAGAAC	2100		SVTIVLVAEAVSPGLIIFTKQKEDSYVCGYFPPRWNNFETIMRNLLGIVPLLIM	
Db	2041	TCTACCTTCAGGCCATCTGGTAAGAGTGGCCAGTGTCTGATGCCAAAGAAC	2100		CESTSOOLDQARQNTEPFLGTMATGTTTGTGATGCCAAAGAAC	
Qy	2101	TTTCACCTTCATATTTGTATGATCCTATGAAATGTAAGTGTGTGT	2160		PGVRPQKVKVTTQGLDGRGKGSIGRAPEASLQDKEA"	
Db	2101	TTTCACCTTCATATTTGTATGATCCTATGAAATGTAAGTGTGTGT	2160		BASE COUNT	602 a
Qy	2161	TGAAATGTAATAACTGTTAACAACTATGTTGGAAATAAACATGGTAAACTA	2220		ORIGIN	464 c
Db	2161	TGAAATGTAATAACTGTTAACAACTATGTTGGAAATAAACATGGTAAACTA	2220		Score 2232; DB 9;	508 g
Qy	2221	TGTGATAAAG 2232			Length 2232;	658 t
Db	2221	TGTGATAAAG 2232			Best Local Similarity 100.0%;	
					Mismatches 0;	
					Indels 0;	
					Gaps 0;	
Qy	1	GGATGAAACAGGAGCCATTCCCACTGATCCACACATGCCACATCTCGCTCT	60			
Db	1	GGATGAAACAGGAGCCATTCCCACTGATCCACACATGCCACATCTCGCTCT	60			
Qy	61	CGGTATTATCAGAAATAACCAACGAGGACCCGCTGAAAGACTGCCAC	120			
Db	61	CGGTATTATCAGAAATAACCAACGAGGACCCGCTGAAAGACTGCCAC	120			
Qy	121	TACGGTGTGTCCTGTCATAAATTGACGTGAGCAAAATTGGGCCAACACTG	180			
Db	121	TACGGTGTGTCCTGTCATAAATTGACGTGAGCAAAATTGGGCCAACACTG	180			
Qy	181	CTCTRACTCGTGTGGTTTCATCTTGGTTGGGAAACATGCTGTCCTCATCTTA	240			
Db	181	CTCTRACTCGTGTGGTTTCATCTTGGTTGGGAAACATGCTGTCCTCATCTTA	240			
Qy	241	ATAAACTGCAAAAGCTGAAGTGTGTACTGACATTTACCTGTCACCTCTCT	300			
Db	241	ATAAACTGCAAAAGCTGAAGTGTGTACTGACATTTACCTGTCACCTCTCT	300			
Qy	301	GATCTGCTTTTCATTTACTCTCCATGTCACCTGTCACCTCTCTCTCTCT	360			
Db	301	GATCTGCTTTTCATTTACTCTCCATGTCACCTGTCACCTCTCTCTCT	360			
Qy	361	TTGGGAATGGCAATGTCGAATTATTCACAGGGCTGTATCACGGTATTTCGGGA	420			
Db	361	TTGGGAATGGCAATGTCGAATTATTCACAGGGCTGTATCACGGTATTTCGGGA	420			
Qy	421	ATCTTCCTCATCTCATCTCATCTCATCTCATCTCATCTCATCTCATCTCAT	480			
Db	421	ATCTTCCTCATCTCATCTCATCTCATCTCATCTCATCTCATCTCATCTCAT	480			
Qy	481	GCTTTAAAGCCAGGAGCTGTCACCTTGGGGTGTACACTGGTTGGTGGTGGT	540			
Db	481	GCTTTAAAGCCAGGAGCTGTCACCTTGGGGTGTACACTGGTTGGTGGTGGT	540			
Qy	541	GCTGTGTTGGCTGCTGTCCTCCAGGAAATCTCTTACTTAATGCCAGAAAGATCTGT	600			
Db	541	GCTGTGTTGGCTGCTGTCCTCCAGGAAATCTCTTACTTAATGCCAGAAAGATCTGT	600			
Qy	601	TATGTCGTGGCCCTTATTTCACAGGAGTGGAAATAATTCCACACATAATGGAAAC	660			

601	TATGTCCTGGCCCTTATTTCACGAGATGGATAATTCCACACATACTAGGAAC	660	Db	1681	CTCTCAGGCTTGGCCAAAGCCTTGTGTCATATTGAACTTATGAACTCATGC 1740	
661	ATTTGGGCTGGCTCCGGCTCATCTGGCATCTGGGAATCTGGAAATCTGAAA	720	Qy	1741	GTTAACACATTGGATGTTTCACTGTTGCTGAGATGTCCTTGTGTCATATTGTTCC 1800	
661	ATTTGGGCTGGCTCCGGCTCATCTGGGAATCTGGAAATCTGGAAATCTGAAA	720	Db	1741	GTTAACACATTGGATGTTTCACTGTTGCTGAGATGTCCTTGTGTCATATTGTTCC 1800	
661	ATTTGGGCTGGCTCCGGCTCATCTGGGAATCTGGAAATCTGGAAATCTGAAA	720	Qy	1801	CTAAATTGCCAGTGGGAACCTCCPAATTCAAATGGCTTCAATCAAGCTTAAACCT 1860	
721	ACCCCTGCTGCTGCTGCTGAAACGAGAAAGGGCATAGGGCACTGAGACTC	780	Db	1801	CTAAATTGCCAGTGGGAACCTCCPAATTCAAATGGCTTCAATCAAGCTTAAACCT 1860	
721	ACCCCTGCTGCTGCTGAAACGAGAAAGGGCATAGGGCACTGAGACTC	780	Qy	1861	ATGGTAAGAATGGTGGAGAGCTCCCTGAAGTAAGCAAGACTTCCCTCTAGT 1920	
781	ATCATGATGTTACTTCTGGCTCTGGTAACTGTGAAACCCAGTCACGGACAC	840	Db	1861	ATGGTAAGAATGGTGGAGAGCTCCCTGAAGTAAGCAAGACTTCCCTCTAGT 1920	
781	ATCATGATGTTACTTCTGGCTCTGGTAACTGTGAAACCCAGTCACGGACAC	840	Qy	1921	CGAGCCAACTTAAGATGGTCTTATGGCCAGTGTCTGATCTGATGCAACCAAG 1980	
841	TTCAGGAAATTCTGGCTCTGGTAACTGTGAAACCCAGTCACGGACAC	900	Db	1921	CGAGCCAACTTAAGATGGTCTTATGGCCAGTGTCTGATCTGATGCAACCAAG 1980	
841	TTCAGGAAATTCTGGCTCTGGTAACTGTGAAACCCAGTCACGGACAC	900	Qy	1981	AAACACTGGCTCTGGAACTTGAAGTGGACTAGACTCCAAAGCTGACTATGGC 2040	
901	CAGGTGACAGAAACTCTGGATGACTCTGGCTCATCAATCTGGCTTC	960	Db	1981	AAACACTGGCTCTGGAACTTGAAGTGGACTAGACTCCAAAGCTGACTATGGC 2040	
901	CAGGTGACAGAAACTCTGGATGACTCTGGCTCATCAATCTGGCTTC	960	Qy	2041	TCTACTTTAGGCCACATGGCTTAAGAAGGGTTCAAGAAGGGTTCAAGAAGAC 2100	
961	GTGGGGGAGACTTGAAGACCTTTTCACATAGCTTGGCTGTAGGATGCCCAACTC	1020	Db	2041	TCTACTTTAGGCCACATGGCTTAAGAAGGGTTCAAGAAGGGTTCAAGAAGAC 2100	
961	GTGGGGGAGACTTGAAGACCTTTTCACATAGCTTGGCTGTAGGATGCCCAACTC	1020	Qy	2101	TTTCACTCTATATTTGTATGATGCTTAATGATGCTTAAATGTTAAAGTGTGAG 2160	
1021	CAAACACCGTGTGGAGGTCCAGGAGTGGACCCAGGAAGAATGACTACA	1080	Db	2101	TTTCACTCTATATTTGTATGATGCTTAATGTTAAATGTTAAAGTGTGAG 2160	
1021	CAAACACCGTGTGGAGGTCCAGGAGTGGACCCAGGAAGAATGACTACA	1080	Qy	2161	TGAATGTAATCTGTTAACACTATGTTAACTGTTAACATGTTAAATGTTAACTA 2220	
1081	CAAGGACTCCUGATGTCGAGTGAACCTTTCACATAGCTTGGCTGTAGG	1140	Db	2161	TGAATGTAATCTGTTAACACTATGTTAACTGTTAACATGTTAACTAATGTTAACTA 2220	
1081	CAAGGACTCCUGATGTCGAGTGAACCTTTCACATAGCTTGGCTGTAGG	1140	Qy	2221	TGTGTAAAG 2232	
1141	CTTCAGGACAAAGGAGCTAGACAAATGACATCUCCTGTTGGAAATTCACA	1200	Db	2221	TGTGTAAAG 2232	
1141	CTTCAGGACAAAGGAGCTAGACAAATGACATCUCCTGTTGGAAATTCACA	1200	Qy	RESULT 4		
1201	CCTGCTGGCTCACAGTGTTGATTCACAGTGTAATGGCTTACAGTTACAGGA	1260	HSMPA02	5471 bp	DNA linear	
1201	CCTGCTGGCTCACAGTGTTGATTCACAGTGTAATGGCTTACAGTTACAGGA	1260	LOCUS	HSMPA02	PRI 24-JUL	
1201	CCTGCTGGCTCACAGTGTTGATTCACAGTGTAATGGCTTACAGTTACAGGA	1260	DEFINITION	Human monocyte chemoattractant protein 1 receptor gene, two alternatively spliced forms, complete cds.		
1261	GCAAGGCTGAGGGAGAGACTCCACGCTGGTTGGAAAACAGCTTCAAACTACCT	1320	ACCESSION	U80924		
1261	GCAAGGCTGAGGGAGAGACTCCACGCTGGTTGGAAAACAGCTTCAAACTACCT	1320	VERSION	U80924.1	GI:17730322	
1321	TCCAGTCCTCATTTGAATACAGGCCATGAGCTTCAAGCTTCAAACTACCT	1380	KEYWORDS			
1321	TCCAGTCCTCATTTGAATACAGGCCATGAGCTTCAAGCTTCAAACTACCT	1380	ORGANISM	Homo sapiens		
1321	TCCAGTCCTCATTTGAATACAGGCCATGAGCTTCAAGCTTCAAACTACCT	1380	DEFINITION	Buteleoston		
1321	TCCAGTCCTCATTTGAATACAGGCCATGAGCTTCAAGCTTCAAACTACCT	1380	LOCATION	Craniata; Chordata; Craniata; Vertebrata; Euteleoston		
1321	TCCAGTCCTCATTTGAATACAGGCCATGAGCTTCAAGCTTCAAACTACCT	1380	DEFINITION	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
1381	AAATATAAGCTGAAACTGCACTTGTAAATGTGTAAGAGTTAGTTGAGTGTCTAT	1440	REFERENCE	1 (bases 1 to 5471)		
1381	AAATATAAGCTGAAACTGCACTTGTAAATGTGTAAGAGTTAGTTGAGTGTCTAT	1440	AUTHORS	Wong, L.M., Myers, S.J., Tsou, C.L., Gosling, J., Arai, H. and Charo, I.F.		
1381	AAATATAAGCTGAAACTGCACTTGTAAATGTGTAAGAGTTAGTTGAGTGTCTAT	1440	TITLE	Organization and differential expression of the human monocyte chemoattractant protein 1 receptor gene. Evidence for the role of the carboxyl-terminal tail in receptor trafficking		
1441	CATGTCAAACGCTGAAATGCTGTTAGTCACAGATACTTCAAGCTTCAAACTACCT	1500	JOURNAL	J. Biol. Chem. 272 (2), 1038-1045 (1997)		
1441	CATGTCAAACGCTGAAATGCTGTTAGTCACAGATACTTCAAGCTTCAAACTACCT	1500	MEDLINE	97150864		
1501	ATTTTGAGGAGGTGGTATGTTGGAGACTGCTGAGTCACCCAACTAGTTGTTGAG	1560	PUBMED	8995400		
1501	ATTTTGAGGAGGTGGTATGTTGGAGACTGCTGAGTCACCCAACTAGTTGTTGAG	1560	REFERENCE	1. 5471		
1561	AGGACTGGAGTGTGCTGATCTGGCCACATTAGCCATTGTGCACTGCACTGCA	1620	AUTHORS	Myers, S.J. and Charo, I.F.		
1561	AGGACTGGAGTGTGCTGATCTGGCCACATTAGCCATTGTGCACTGCACTGCA	1620	TITLE	/organism="Homo sapiens"		
1621	ATGATGTCGTTGATCACGTTAGCTGCTCATGCTGAGTGTGATGTTGAGTGT	1680	JOURNAL	/db_xref="taxon:9606"		
1621	ATGATGTCGTTGATCACGTTAGCTGCTCATGCTGAGTGTGATGTTGAGTGT	1680	FEATURES	Direct Submission		
1681	CTCTCAGGCTGGTGTGCTGCCAAAGCCTTGTGTTGATGTCAGCTGAGTCATGC	1740	source	Submitted (04-DEC-1996)		
1681	CTCTCAGGCTGGTGTGCTGCCAAAGCCTTGTGTTGATGTCAGCTGAGTCATGC	1740	Db	Emory University, 1510 Clifton Road, Atlanta, 30322, USA		
Qy	1621	ATGATGTCGTTGATCACGTTAGCTGCTCATGCTGAGTGTGATGTTGAGTGT	1680	Db	/product="monocyte chemoattractant protein 1 receptor A-form carboxy	
Qy	1621	ATGATGTCGTTGATCACGTTAGCTGCTCATGCTGAGTGTGATGTTGAGTGT	1680	Db	/note="alternatively spliced form with A-form carboxy	

BASE COUNT	41194	a	/ab_xref="taxon:9606"	30122	c	32403	g	39349	t
ORIGIN									
Query Match	51	6%	Score 1152;	DB 6;	Length 143068;				
Best Local Similarity	99.8%	pred. No. 0;							
Matches 1252;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;					
Qy	979	AGCCUTTTACATAGCTCTGGCTGATTGCCCACTCCAAAACAGCTGTGGA	1038	Db	49213	ttctatgtgtccccgtgtttcgatctgtggacttggaaacatactggctttctaga	49272		
Db	48253	AGCCUTTTACATAGCTCTGGCTGATTGCCCACTCCAAAACAGCTGTGGA	48312	Qy	1999	ACCAAGCAACTTGGAACTAGACTCCAAAGCTGGACTATGGCTACTTCAGGCCACAT	2058		
Qy	1039	GGTCAGGAGTGTGAGCCGAAAGATGAAAGTGTGAAAGTGTGAAATGTGTT	1098	Db	49273	ACCAAGCAACTTGGAACTAGCTCCAAAGCTGGACTATGGCTACTTCAGGCCACAT	49332		
Db	48313	GGTCAGGAGTGTGAGCCGAAAGATGAAAGTGTGAAATGTGAAATGTGTT	48372	Qy	2059	GGCTAAAGAGGTTCAGAAAGAAAGTGGGACAGAGCAGACTTCACCTTCATATAATT	2118		
Qy	1099	CCTGAAAGGAAAGTCAUTGGAGCCGAAAGTGTGAACTACAGGACTCCTCGATG	1158	Db	49333	GGCTAAAGAGGTTCAGAAAGAAAGTGGGACAGAGCAGACTTCACCTTCATATAATT	49392		
Db	48373	CCTGAAAGGAAAGTCAUTGGAGCCGAAAGTGTGAACTACAGGACTCCTCGATG	48432	Qy	2119	GTTGATCCTTAATGAAATGCTTAAAGTGTGAAATGTGAAATGTGAAATGTGTT	2178		
Qy	1159	GCCTAGAGCAGAAATGAGACATCTCTGTTACGGCAGGCTCTAGGAGAG	1218	Db	49339	GTTGATCCTTAATGAAATGTGAAATGTGAAATGTGAAATGTGAAATGTGTT	49452		
Db	48433	GCCTAGAGCAGAAATGAGACATCTCTGTTACGGCAGGCTCTAGGAGAG	48492	Qy	2179	TTAACACATGATGTTGGAAATAATCACTGCTTAAACATGCTTAACTGTGAAATGTGTT	2232		
Qy	1219	TGTGATCACAGTGTAACTCTGGCTCTACGTTACGGCAGGAGCTGAGGAGAG	1278	Db	49453	TTAACACATGATGCTTAAACATGCTTAACTGTGAAATGTGAAATGTGTT	49506		
Db	48493	TGTGATCACAGTGTAACTCTGGCTCTACGTTACGGCAGGAGCTGAGGAGAG	48552	RESULT	6				
Qy	1279	AACTCCAGCGGGTGGAAACAGTATTCCAAACTACCTTCCATTCTCATTGT	1338	HSU95626	HSU95626	HSU95626			
Db	48553	AGACTCCAGCGGGTGGAAACAGTATTCCAAACTACCTTCCATTCTCATTGT	48612	LOCUS	HSU95626	HSU95626	HSU95626		
Qy	1339	AATACAGCCATAGTGTAGCTTAAAGTAAATTAACCTGAAAC	1398	DEFINITION	HSU95626	HSU95626	HSU95626		
Db	48613	AATACAGCCATAGTGTAGCTTAAAGTAAATTAACCTGAAAC	48672	ORGANISM	HSU95626	HSU95626	HSU95626		
Qy	1399	TGCAACTTGTAAATGTGCTAAAGGTTAGCTCATGTCAACTGAAAT	1458	REFERENCE	1	1	1		
Db	48613	TGCAACTTGTAAATGTGCTAAAGGTTAGCTCATGTCAACTGAAAT	48732	AUTHORS	1	1	1		
Qy	1459	GCTGTTATGTCACAGAGATAATTCTGTTGAGCTTAAGATTGTGTT	1518	TITLE	1	1	1		
Db	48733	GCTGTTATGTCACAGAGATAATTCTGTTGAGCTTAAGATTGTGTT	48792	JOURNAL	1	1	1		
Qy	1519	GTTGGGAGACTGTGATCACCCATTAGTTGTTGAGCTGGAACTGTG	1578	COMMENT	1	1	1		
Db	48793	GTTGGGAGACTGTGATCACCCATTAGTTGTTGAGCTGGAACTGTG	48852	FEATURES	1	1	1		
Qy	1579	ATCGTGGCACATTAGCCATTAGCTATGGCATTAGCTTAATGATG	1638	source	1	1	1		
Db	48853	ATCGTGGCACATTAGCCATTAGCTATGGCATTAGCTTAATGATG	48912	organism	1	1	1		
Qy	1639	CAGTATCGTCCATGCTTCACTGCTCATGCTTCACTGCTTCACTG	1698	db_xref	1	1	1		
Db	48913	CAGTATCGTCCATGCTTCACTGCTCATGCTTCACTGCTTCACTG	48972	chromosome	1	1	1		
Qy	1699	AAAGCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1758	clone	1	1	1		
Db	48973	AAAGCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	49032	gene	1	1	1		
Qy	1759	GTTCAGTGTGTTGAGCTGCTCATATTGTTCCATTGCTTCACTGCTT	1818	note	1	1	1		
Db	49033	GTTCAGTGTGTTGAGCTGCTCATATTGTTCCATTGCTTCACTGCTT	49092	note	1	1	1		
Qy	1819	CTCCCTAAATCAATGCTTAAAGCTTAAACCTTATGGAAAGTGGAAAG	1878	note	1	1	1		
Db	49093	CTCCCTAAATCAATGCTTAAAGCTTAAACCTTATGGAAAGTGGAAAG	49152	note	1	1	1		
Qy	1819	GTGGAGAGTCCCTGAGTAAAGCTTCCATTGCTTCACTGCTTCACTG	1938	note	1	1	1		
Db	49153	GTGGAGAGTCCCTGAGTAAAGCTTCCATTGCTTCACTGCTTCACTG	49212	note	1	1	1		
Qy	1939	TTCTTATGTTGCCAGTGTGTTCTGATGCAAGAACAAACATGGCTTCTAGA	1998	note	1	1	1		

QY	1219	TGTGATTACAGTGTGAATCTTGGTCTACGTACAGGGCTGAGGGAGAG 1278	ACCESSION VERSION KEYWORDS SOURCE	G07239.1 GI:860484 STS sequence; primer; sequence tagged site.
Db	16444	TGTGATTACAGTGTGAATCTTGGTCTACGTACAGGGCTGAGGGAGAG 16503	ORGANISM	Homo sapiens STSs derived from sequences in dbEST and the Unigene collection.
QY	1279	AGACTCAGGTGGTGGAAAACAGTATTTACCAACTACCTCCAGTCTCACTTTG 1338	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 1068)
Db	16504	AGACTCAGGTGGTGGAAAACAGTATTTACCAACTACCTCCAGTCTCACTTTG 16563	AUTHORS	Hudson,T.
QY	1339	AATACAGGATAGAGTCAAGCTTTTAATATTAATAAACTAAAGCTGAAAC 1398	TITLE	Whitehead Institute/MIT Center for Genome Research; Physically Mapped ESTs
Db	16564	AATACAGGATAGAGTCAAGCTTTTAATATTAATAAACTAAAGCTGAAAC 16623	JOURNAL	unpublished (1995)
QY	1399	TGCAACTTGTAAATGTTAAAGAGTTAGTTGACTCAAGCTGAAAT 1458	COMMENT	Contact: Thomas Hudson Whitehead Institute/MIT Center for Genome Research Whitehead Institute for Biomedical Research 9 Cambridge Center, Cambridge MA 02142 USA Tel: 617 252 1900 Fax: 617 252 1902 Email: thudson@gene.wi.mit.edu
Db	16624	TGCAACTTGTAAATGTTAAAGAGTTAGTTGACTCAAGCTGAAAT 16683	Primer A:	GGAAATCACCCCTCTGGCTT
QY	1459	GCTGTATTAGTCACAGAGATAATTCTGCTTGTAGATTGAGCTTGCTGTAT 1518	Primer B:	ACTGTTTCCACCCAGCTG
Db	16684	GCTGTATTAGTCACAGAGATAATTCTGCTTGTAGATTGAGCTTGCTGTAT 16743	STS size:	114
QY	1519	GTTGGGGAGCTGACTCTGACTCAACCCAACTAGTTGATTTGGAGGTGGTGT 1578	PCR Profile:	Presok:
Db	16744	GTTGGGGAGCTGACTCTGACTCAACCCAAATAGTTGATTTGGAGGTGGTGT 16803	Denaturation:	Denaturation: 56 degrees C
QY	1579	ATCTGTGGCACATTAGCTAATGCTAGTCATGCACTTGTGTTGAATCA 1638	Polymerization:	Primer: each 10 ng
Db	16804	ATCTGTGGCACATTAGCTAATGCTAGTCATGCACTTGTGTTGAATCA 16863	PCR Cycles:	DNTPs: each 4 nM
QY	1639	CAGTATAGCGCTCATCGCTGCTGATCTGGATCTGCATCTGGCTGCGCA 1698	Tag Polymerase:	Tag Polymerase: 0.025 units/ul
Db	16864	CAGTATAGCGCTCATCGCTGCTGATCTGGATCTGCATCTGGCTGCGCA 16923	Total Vol:	Total Vol: 20 ul
QY	1699	AAAGCCTTGTGGTTGATCATATGAGTGTATGCTCATTTGCTGGACT 1758	Buffer:	Buffer: MgCl ₂ : 1.5 mM
Db	16924	AAAGCCTTGTGGTTGATCATATGAGTGTATGCTCATTTGCTGGACT 16983	Primer:	Primer: each 5 pM
QY	1759	GTTTCACTGCTTCGAGATGCCCTGATCTGCTCATTTGCTGGACT 1818	Tris-HCl:	Tris-HCl: 10 mM
Db	16984	GTTTCACTGCTTCGAGATGCCCTGATCTGCTCATTTGCTGGACT 17043	PH:	PH: 9.3
QY	1819	CCTCTAAATCAAATGCGCTCTAACTCAAGCTTAAACCTATGGTCCATTTGCTGGAG 1878	FEATURES	Prepared with primer pairs derived from U03892 -- Unigene.
Db	17044	CCTCTAAATCAAATGCGCTCTAACTCAAGCTTAAACCTATGGTCCATTTGCTGGAG 17103	source	Location/Qualifiers
QY	1879	GTGGGAAAGCTCTGAGTCTAGTCTAGCTTAAAGCTTAAAGCTTAAAGATG 1938	1..1068	1..1068
Db	17104	GTGGGAAAGCTCTGAGTCTAGCTTAAAGCTTAAAGCTTAAAGATG 17163	/organism="Homo sapiens"	/db_xref="taxon:9606"
QY	1939	TCTCTATGTTGCCCCAGTGTGTTCTGATCTGATGAAAGCTGGCTCTCTAGA 1998	/map="730_D5; 913_C_5; 941_A_7; 743_H_10; 781_B_10;	/map="730_D5; 913_C_5; 941_A_7; 743_H_10; 781_B_10;
Db	17164	TCTCTATGTTGCCCCAGTGTGTTCTGATCTGATGAAAGCTGGCTCTCTAGA 17223	STS	STS
QY	1999	ACCCGCAACTGGGAACTAGACTCCAAAGCTTAAAGCTTAAATCTGTT 2058	primer_bind	primer_bind
Db	17224	ACCCGCAACTGGGAACTAGACTCCAAAGCTTAAATCTGTT 17283	primer_bind	primer_bind complement (121..140)
QY	2059	GGCTAAAGAAAGCTTCAAGAAAGCTTCAAGCTTCACTCTATATT 2118	BASE COUNT	BASE COUNT 315 a 186 c 238 g 329 t
Db	17284	GGCTAAAGAAAGCTTCAAGAAAGCTTCACTCTATATT 17343	ORIGIN	ORIGIN
QY	2119	GTATGATCTTAATGAACTCATAAAATGTTAAGTGTGATGAAATGTAATACTGTT 2178	Query Match	Query Match 47.8%; Score 1068; DB 11; Length 1068;
Db	17344	GTATGATCTTAATGAACTCATAAAATGTTAAGTGTGATGAAATGTAATACTGTT 17403	Best Local Similarity	Best Local Similarity 100.0%; Pred. No. 0;
QY	2179	TTAACACACTATGTTGAAATAATCAATGCTTAAACTATGTTGATGAAATGTAATACTGTT 2232	Mismatches	Mismatches 0; Mismatches 0; Indels 0; Gaps 0;
Db	17404	TTAACACACTATGTTGAAATAATCAATGCTTAAACTATGTTGATGAAATGTAATACTGTT 17457	Matches	Matches 100%; Conservation
RESULT	8			
G07239	G07239			
LOCUS	human STS WI-9314	1068 bp	DNA	sequence tagged site.
DEFINITION	human STS WI-9314	1068 bp	DNA	sequence tagged site.

Qy	1345	GGCATAGAGTTGAGACUTTTTAATTAGTAATAAATTAAATTAAAGCTGAAACTGCAAC	1404
Db	181	GGCATAGAGTTGAGACUTTTTAATTAGTAATAAATTAAATTAAAGCTGAAACTGCAAC	240
Qy	1405	TTGTAATCTGTAAAGAGTAGTTGAGTTGCTATGCAACAGTAAATTAGCTGAAACTGCAAC	1464
Db	241	TTGTAATCTGTAAAGAGTAGTTGAGTTGCTATGCAACAGTAAATTAGCTGAAACTGCAAC	300
Qy	1465	TTAGTCACAGAGATAATTCTAGCTTTGAGCTTAAAGAATTGAGCAGGTGTTATGTTGG	1524
Db	301	TTAGTCACAGAGATAATTCTAGCTTTGAGCTTAAAGAATTGAGCAGGTGTTATGTTGG	360
Qy	1525	GAGACTGCTGAGTCACCCAAATACTGTGATTCAGGAGTTGAACTGTTGATCTGT	1584
Db	361	GAGACTGCTGAGTCACCCAAATACTGTGATTCAGGAGTTGAACTGTTGATCTGT	420
Qy	1585	GGGCACATTAAGCCATTAGCTCATGTCATGAGCATCTAAAGTAATGTCGTTGAATCACAGTAT	1644
Db	421	GGGCACATTAAGCCATTAGCTCATGTCATGAGCATCTAAAGTAATGTCGTTGAATCACAGTAT	480
Qy	1645	ACGCTCCATGCCCTGTCATCTAGGGATCTCCATTCTCAGGCTGCTGCAAAAGCC	1704
Db	481	ACGCTCCATGCCCTGTCATCTAGGGATCTCCATTCTCAGGCTGCTGCAAAAGCC	540
Qy	1705	TTTGTGTTGTTGTATCATTTGAGCTCATTTGAGCTCATTTGCTTAACTCACATTGCGAGTTCTA	1764
Db	541	TTTGTGTTGTTGTATCATTTGAGCTCATTTGAGCTCATTTGCTTAACTCACATTGCGAGTTCTA	600
Qy	1765	GTGCTTCGGAGATGTTGATGCTCATATTGCTTAACTTCAGGTTCTCAGGTTCTA	1824
Db	601	GTGCTTCGGAGATGTTGATGCTCATATTGCTTAACTTCAGGTTCTCAGGTTCTA	660
Qy	1825	AATCAAAATTGGCTTCAATCAAAAGCTTAAACCCATTGTTAAAGTAATGCAAGTTGGAG	1884
Db	661	AATCAAAATTGGCTTCAATCAAAAGCTTAAACCCATTGTTAAAGTAATGCAAGTTGGAG	720
Qy	1885	AAAGCTCCCTGAAAGAAAGCTTCCCTTAACTGAGCCAAACTTAAGAATGTTCTTA	1944
Db	721	AAAGCTCCCTGAAAGAAAGCTTCCCTTAACTGAGCCAAACTTAAGAATGTTCTTA	780
Qy	1945	TGTGCCCCAGTTGTTCTGATCTGATGCAAGCAAGAAACACTGGCTCTAGACCAAGG	2004
Db	781	TGTGCCCCAGTTGTTCTGATCTGATGCAAGCAAGAAACACTGGCTCTAGACCAAGG	840
Qy	2005	CAACTGGGAACTAGACTTCCCAAGCTGGACTATGGCTCTACTTCAGGCCACATGGCTA	2064
Db	841	CAACTGGGAACTAGACTTCCCAAGCTGGACTATGGCTCTACTTCAGGCCACATGGCTA	900
Qy	2065	AGAAAGTTCTGAAAGAAAGCTGGGAACAGCCAGACTTCACCCCTATATTTGTATGA	2124
Db	901	AGAAAGTTCTGAAAGAAAGCTGGGAACAGCCAGACTTCACCCCTATATTTGTATGA	960
Qy	2125	TCCTTAATGAACTGCTAAATTAGTTAGTTGATGTTGATGAAAGTAAACTGTTTAAAC	2184
Db	961	TCCTTAATGAACTGCTAAATTAGTTAGTTGATGTTGATGAAAGTAAACTGTTTAAAC	1020
Qy	2185	AACTGATTTGGAAATAAAATCAATGCTTAACTATGTTGATAAAAG	2232
Db	1021	AACTGATTTGGAAATAAAATCAATGCTTAACTATGTTGATAAAAG	1068

AUTHORS	Charo, I.F. and Coughlin, S.R.
TITLE	Recombinant mammalian monocyte chemotactic protein-1 (MCP-1)
JOURNAL	receptors (MCP-1R, CCR-2)
FEATURES	Patent: US 6132987-A 3 17-OCT-2000;
source	Location/Qualifiers 1..1979 /organism="unknown"
BASE COUNT	530 a 435 c 451 g 563 t
ORIGIN	
Query Match	43.9%
Best Local Matches	100.0%
Best Local Matches	980; Conservative 0; Pred. No. 0;
Indels	0; Gaps
Qy	1 GGATGAAAGGACCCATTCCCGAGTACATCCACAAATGCTGTCACACATCTGCTTCT 60
Db	42 GGATGAAAGGACCCATTCCCGAGTACATCCACAAATGCTGTCACACATCTGCTTCT 10
Qy	61 CGGTTATCAGAAATACCAACGAGAACGGTGGAAAGTCAACCCCTTTGATATTGAT 124
Db	102 CGGTTATCAGAAATACCAACGAGAACGGTGGAAAGTCAACCCCTTTGATATTGAT 16
Qy	121 TACCGTGCCTCTTCATAAATTGACGTTGAAAGCAATTGGGCCAACCTGCTCTCCG 184
Db	162 TACCGTGCCTCTTCATAAATTGACGTTGAAAGCAATTGGGCCAACCTGCTCTCCG 224
Qy	181 CTCTACTGGGTTCTCTTGTGGCAACATGCTGGTCTCTGATCTTCTCTCTCTCTCT 244
Db	222 CTCTACTCTGGTTCTCTTGTGGCAACATGCTGGTCTCTCTCTCTCTCTCTCTCT 281
Qy	241 ATAACTGAAAGCTGAAAGTGGTTGACTGACATTACTCTGGCTCAACTCTGGCCATCTCT 300
Db	282 ATAACTGAAAGCTGAAAGTGGCTCAACTCTGGCCATCTCTCTCTCTCTCTCTCTCT 341
Qy	301 GATCTGCTTTCTTCTTACTCTCCATTACTCTGGCTCAATGTTGCTGAAATGTTGGCTC 360
Db	342 GATCTGCTTTCTTCTTACTCTCCATTACTCTGGCTCAACTCTGGCTCAATGTTGGCTC 401
Qy	361 TTGGGATGCAATGTCGAATTATTCACAGGGCTGTATCACATGGTTATTTGGCGA 420
Db	402 TTGGGATGCAATGTCGAATTATTCACAGGGCTGTATCACATGGTTATTTGGCGA 461
Qy	421 ATCTCTTCATCATCCCTCTGACAATCTGATAGATACCTGGTATGTCATGCTGTTT 480
Db	462 ATCTCTTCATCATCCCTCTGACAATCTGATAGATACCTGGTATGTCATGCTGTTT 521
Qy	481 GCTTTAAAGCCAGGAGGGTCACTTTGGGTGTCAGAAGTGTGATCACCTGGTGGT 540
Db	522 GCTTTAAAGCCAGGAGGGTCACTTTGGGTGTCAGAAGTGTGATCACCTGGTGGT 581
Qy	541 GCTGTGTTCTCTGTCCTCCAGGAATCATCTTCTAATGCCAGAAAGAGATCTGTT 600
Db	582 GCTGTGTTCTCTGTCCTCCAGGAATCATCTTCTAATGCCAGAAAGAGATCTGTT 641
Qy	601 ATGTCGTGCGCTTATTCACAGGATGAAATAATTCCACAAATATGGGAAC 660
Db	642 ATGTCGTGCGCTTATTCACAGGATGAAATAATTCCACAAATATGGGAAC 701
Qy	661 ATTTGGGTGGCTCTGGCTCATGTCATCTGCTACTCTGGAAATCTGAA 720
Db	702 ATTTGGGTGGCTCTGGCTCATGTCATCTGCTACTCTGGAAATCTGAA 761
Qy	721 ACCCTGCTTCGCGCTGTCGAAAGCAGAAAGAGGGCATAGGGCACTGAGTCATCTCACC 780
Db	762 ACCCTGCTTCGCGCTGTCGAAAGCAGAAAGAGGGCATAGGGCACTGAGTCATCTCACC 821
Qy	781 ATCATGATGTTACTTCTGGCTGACTAATGCCAGAAAGATCTGAA 840
Db	822 ATCATGATGTTACTTCTGGCTGACTAATGCCAGAAAGATCTGAA 881
Qy	841 TTCCAGGAAATTCTGGCTGACTAATGCCAGAAAGATCTGAACTGGCCAG 900
Db	882 TTCCAGGAAATTCTGGCTGACTAATGCCAGAAAGATCTGAACTGGCCAG 941

QY	901	CAGGTGACAGAGACTCTGGGAGGACTCACTGGCATCAATGCCATCATCTATGCCPTC	960	Db	582	GCTGTGTTGCTTCGTCGCCAGGAAATCATCTTACTAAATGCCAGAAAGAGATTCTGTT	641
Db	942	CAGGTGACAGAGACTCTGGGATGACTCATCTGGCATCAATGCCATCATCTATGCCPTC	1001	Qy	601	TATGCTGTGTCGCCCTATTTTCCAGGGATGAAATAATTCCAGACAATAATGGGAAC	660
Qy	961	GTGGGGAGAAGAGTCAGAG 980		Db	642	TATGCTGTGTCGCCCTATTTTCCAGGGATGAAATAATTCCAGACAATAATGGGAAC	701
Db	1002	GTGGGGAGAAGAGTCAGAG 1021		Qy	661	ATTTGGGGCTGGCTGGCCCTGTCATGGCATCTGGTACTCTGGGAATCTCGAA	720
RESULT	10			Db	702	ATTTGGGGCTGGCTGGCCCTGTCATGGCATCTGGTACTCTGGGAATCTCGAA	761
LOCUS	179543	179543	1979 bp	DNA	linear	PAT 10-JUN-1998	
DEFINITION	Sequence 3 from patent us 5707815.			Qy	721	ACCCCTCTTCCTGGTCAAAGGAGAAAGGCAATGGGAGTGGAGAGTCATCTTC	780
ACCESSION	I179543	I179543		Db	762	ACCCCTCTTCCTGGTCAAAGGAGAAAGGCAATGGGAGTGGAGAGTCATCTTC	821
KEYWORDS				Qy	781	ATCATGATGTTTACCTTCTGGACTCCTATAACATGTCATTCTCGAACAC	840
SOURCE	Unknown.			Db	822	ATCATGATGTTTACCTTCTGGACTCCTATAACATGTCATTCTCGAACAC	881
ORGANISM	Unclassified.			Qy	841	TTCAGGAATCTTCGGCTCTGTAATCTGTGAAAGCACCACATGGGAAAGGCCAC	900
REFERENCE	1 (bases 1 to 1979)			Db	882	TTCAGGAATCTTCGGCTCTGTAATCTGTGAAAGCACCACATGGGAAAGGCCAC	941
AUTHORS	Charo, I.F. and Coughlin, S.R.			Qy	901	CAGGTGACAGAGACTCTGGGATGACTCACTGCTGCCATCAATCCATCATCTATGCCCTC	960
TITLE	Mammalian monocyte chemoattractant protein receptors and assays using them			Db	942	CAGGTGACAGAGACTCTGGGATGACTCACTGCTGCCATCAATCCATCATCTATGCCCTC	1001
JOURNAL	Patent: US 5707815-A 3 13-JAN-1998;			Qy	961	GTTGGGAGAAGTCAGAG 980	
FEATURES	Location/Qualifiers			Db	1002	GTTGGGAGAAGTCAGAG 1021	
SOURCE	1..1979 /organism="unknown"			RESULT	11		
BASE COUNT	530 a 435 c 451 g 563 t			HSU03905			
ORIGIN				LOCUS		HSU03905	
Query Match	43.9%	Score 980;	DB 6;	DEFINITION		1799 bp mRNA	PRI 22-JUN-1994
Best Local Similarity	100.0%	Pred. No: 0;	Mismatches 0;	ORGANISM		Human monocyte chemoattractant protein 1 receptor (MCP-1RB)	
Matches 980;	Conservative	Indels 0;	Gaps 0;	DEFINITION		alternative spliced mRNA, complete cds.	
Qy	1	GGATTGACAAAGGACGATTTCCCGATCATCACACATGTCACATCTCGCTCT	60	ACCESSION	U03905		
Db	42	GGATTGACAAAGGACGCTTTCCCGATCACATGTCACATCTCGCTCT	101	VERSION	1		
Qy	61	CGGTTATGAAATAACGACGAGGCTGAAAGCTACCACTTTGATTATAT	120	KEYWORDS	GT1:472557		
Db	102	CGGTTATGAAATAACGACGAGGCTGAAAGCTACCACTTTGATTATAT	161	SOURCE	human.		
Qy	121	TACGGTGCCTCCCTCATTAATTGACCTGAACTGGGCCAACTCTGGCTCG	180	ORGANISM	Homo sapiens		
Db	162	TACGGTGCCTCCCTCATTAATTGACCTGAACTGGGCCAACTCTGGCTCG	221	DEFINITION	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;		
Qy	181	CTCTACTCGCTGGCTCATCTTGGTATTGTCGGCACACATGCTGGCTCCATCTTA	240	REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
Db	222	CTCTACTCGCTGGCTCATCTTGGTATTGTCGGCACACATGCTGGCTCCATCTTA	281	AUTHORS	1. (bases 1 to 1979)		
Qy	241	ATAAACTGAAAAGCTGAACTTACTGCAATTACTGCTGCAACACTGCTCT	300	TITLE	Charo, I.F., Myers, S.J., Herman, A., Franci, C., Connolly, A.J. and Coughlin, S.R.		
Db	282	ATAAACTGCAAAAAGCTGAACTTACTGCTGCAACACTGCTCT	341	JOURNAL	Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors reveals alternative splicing of the carboxy-terminal tails		
Qy	301	GATCTGCTTTCTCATTAATCTCCATTTGGCTACTCTGCTGCAAATGAGTGGCTC	360	JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 91 (7), 2752-2756 (1994)		
Db	342	GATCTGCTTTCTCATTAATCTCCATTTGGCTACTCTGCTGCAAATGAGTGGCTC	401	FEATURES	JOURNAL MEDLINE		
Qy	361	TTTGGGATGCGAATGTCGAATTATTCACAGGGCTACTCTGGCTTATTTGGGAA	420	source	81495821		
Db	402	TTTGGGATGCGAATGTCGAATTATTCACAGGGCTACTCTGGCTTATTTGGGAA	461	REFERENCE	814816		
Qy	421	ATCTCTCTCATCTCCCTGCAAACTGCTGCAATGCTGCTGCTGCTGCTGCTG	480	AUTHORS	2 (bases 1 to 1979)		
Db	462	ATCTCTCTCATCTCCCTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG	521	TITLE	Myers, S.J.		
Qy	481	GCTTAAAGCCAGGAGGTCACTTGGCTTATGGTACAATGGTACACTGGTGGTGG	540	JOURNAL	Direct Submission		
Db	522	GCTTAAAGCCAGGAGGTCACTTGGCTTATGGTACAATGGTACACTGGTGGTGG	581	FEATURES	Submitted (02-DEC-1993) Scott J. Myers, Cardiovascular, The Gladstone Institutes, 2550 23rd Street, San Francisco, CA 94110, USA		
Qy	541	GCTGTGTTGCTTCGTCGCCAGGAATATCTTACTPAATGCCAGAAAGATTCTGTT	600	source	Location/Qualifiers		

QY	580	TGCCAGAAAGAGATTCTGTTATGCTGTCGCCCTTATTTCACAGGAGTGGATAAT	639	280	CTGCTCAACCTGGCCATCTGATCTGCTTCTTCTTATTACTCTCCATTGTCATGGGCTCAC	339	
QY	541	TGCCAGAAAGAGATTCTGCTTATGCTGTCGCCCTTATTTCACAGGAGTGGATAAT	600	241	CTGCTCAACCTGGCCATCTGATCTGCTTCTTATTACTCTCCATTGTCATGGGCTCAC	300	
Db	640	TGCCAGAAATATGAGAACATTGGGGTCTCTGGCTGCTGTCATGGTCATC	699	340	TCTCTGCAAAATTGAGTGGATGCAATGTCAAATTATTCAAGGGCTGTAT	399	
Db	601	TGCCAACAAATGAGAACATTGGGGTCTCTGGCTGCTGTCATGGTCATC	660	301	TCTCTGCAAAATTGAGTGGCTTGGGAAATTATTCAAGGGCTGTAT	360	
Db	700	TGCTACTCGGGATTCCTGAAACCTGCTCTGGTCAAAAGAGAGAGGGCATAGG	759	400	CACATGGGTTATTGGCAATCTCTCATCCTGACAAATCGATAATGACATTCTG	459	
Db	661	TGCTACTCGGGATTCCTGAAACCTGCTCTGGTCAAAAGAGAGGGCATAGG	720	361	CACATGGGTTATTGGCAATCTCTCATCCTGACAAATCGATAATGACATTCTG	420	
Db	760	GCAGTGGAGAGTCACTTCACCATCATGATTGTTACCTTCCTGACTCCCTATAAC	819	460	GCTATTGTCATGGCTGTTGCTTAAAGCCAGGACGGTACACCTTGGGGTGGGAGCA	519	
Db	721	GCAGTGGAGAGTCACTTCACCATCATGATTGTTACCTTCCTGACTCCCTATAAC	780	421	GCTATTGTCATGGCTGTTGCTTAAAGCCAGGACGGTACACCTTGGGGTGGGAGCA	480	
Ddb	820	ATTCGTCATCTCTGAAACCTTCACCATCATGATTGTTACCTTCCTGACTCCCTATAAC	879	520	AGTGTGATCACTGGTGGTGTGCTGTTGCTTCTCTGTCAGGAATCTCTTACTAA	579	
Qy	781	ATTCGTCATCTCTGAAACCTTCACCATCATGATTGTTACCTTCCTGACTCCCTATAAC	840	Qy	580	TGCCAGAAAGAGATTCTGTTATGCTGTCGCCCTTATTTCACAGGATGGATAAT	639
Db	880	AGTCACACTGGACCAAGCCACGAGCTGACAGACTCTGGGATGACTCACTGGTCATC	939	Db	481	AGTGTGATCACTGGTGGCTGTTGCTTCTGTCAGGAATCTCTTACTAA	540
Db	841	AGTCACACTGGACCAAGCCACGAGCTGACAGACTCTGGGATGACTCACTGGTCATC	900	Qy	541	TGCCAGAAAGAGATTCTGTTATGCTGTCGCCCTTATTTCACAGGATGGATAAT	600
Db	940	AATCCCATCATCTATGCTCTGTTGGGAGAAGTTCTAGAAG	980	Qy	640	TTCACACAAATTGAGAACATTGGGGCTGTTGCTGCTGTCATCATGGTCATC	699
Db	901	AATCCCATCATCTATGCTCTGTTGGGAGAAGTTCTAGAAG	941	Db	601	TTCACACAAATTGAGAACATTGGGGCTGTTGCTGCTGTCATCATGGTCATC	660
Db				Qy	700	TGGTACTCGGGATCTGAAACCCCTGCTGTCAAACCGAGAAAGGAGGCTAGG	759
Db				Db	661	TGCTACTCGGGATTCCTGAAACCCCTGCTGTCAAACCGAGAAAGGCTAGG	720
RESULT 13	AX32506	1083 bp	DNA	QY	760	GCAGTGGAGTCACTTCACATCATGATTGTTACTTTCTCTGGACTTCCTATAAC	819
LOCUS	AX32506	from Patent	W00162796.	Db	721	GCAGTGGAGTCACTTCACATCATGATTGTTACTTTCTCTGGACTTCCTATAAC	780
DEFINITION	Sequence 1			Qy	820	ATGGTCACTTCCTGAGGATTCCTGGCTGTTACTCTGTTACTCTGAGGAC	879
ACCESSION	AX32506			Db	781	ATGGTCACTTCCTGAGGATTCCTGGCTGTTACTCTGAGGAC	840
VERSION	AX32506..1	GI:15592569		Qy	880	AGTCACACTGGACCAAGCCACGAGCTGACAGACTCTGGGATGACTCACTGTCATC	939
KEYWORDS	human.			Db	841	AGTCACACTGGACCAAGCCACGAGCTGACAGACTCTGGGATGACTCACTGTCATC	900
ORGANISM	Homo sapiens			Qy	940	AATCCCATCATCTATGCTCTGTTGGGAGAAGTTCTAGAAG	980
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			Db	901	AATCCCATCATCTATGCTCTGTTGGGAGAAGTTCTAGAAG	941
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
REFERENCE	1 (bases 1 to 1083)						
AUTHORS	Valdes, A.M., Groot, P.H. and Spurk, N.K.						
TITLE	CCR2-64i, polymorphic variant of the human ccr2 receptor and its use in the diagnostic and treatment of atherosclerosis						
JOURNAL	Patent: WO 0162796-A 1301-08-2001;						
FEATURES	SMITHKLINE BECHAM PLC (GB)						
source	Location/Qualifiers						
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BASE COUNT	256	a	246	321	t		
ORIGIN							
Query Match	39.9%	Score 890; DB 6; Length 1083;					
Best Local Similarity	39.9%	Pred. No. 0; Mismatches 1; Indels 0; Gaps 0;					
Matches	940;	Conservative 0;					
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Db	1	ATGGTGTCCACATCTGCTGTTCTGGTTTATCAGAAATACTAACCGAGACGGTGAAGAAC	60				
Qy	100	ACCACTTGTGTTATGATTAGCTGGTCTGCCCTGTCATAAATTGACCTGAAACAAATT	159				
Db	61	ACCACTTGTGTTATGATTAGCTGGTCTGCCCTGTCATAAATTGACCTGAAACAAATT	120				
Qy	160	GGGCCCAACTCTGCCCTCGTACTGCTGGTTCATCTGGTTGTCATCTGGCAAC	219				
Db	121	GGGCCCAACTCTGCCCTCGTACTGCTGGTTCATCTGGTTGTCATCTGGCAAC	180				
Qy	220	ATGCCGGTGTCTCATCTTAATAACTCTGAAAGCTGAGTGTACTGACATTAC	279				
Db	181	ATGCCGGTGTCTCATCTTAATAACTCTGAAAGCTGAGTGTACTGACATTAC	240				

AUTHORS	Yamagami, S.
TITLE	Direct Submission
COMMENT	Submitted (22-APR-1994) Shinsuke Yamagami, TEIJIN LIMITED, Institute for Bio-Medical Research; 4-3-2 Asahigaoka, Hino, Tokyo 191, Japan (Tel:0425-86-8282)
COMMENT	Submitted (22-Apr-1994) to DBU by: Shinsuke Yamagami Teijin Limited Institute for Bio-Medical Research 4-3-2 Asahigaoka Hino, Tokyo 191 Japan
FEATURES	<p>Phone: 0425-86-8282 Fax: 0425-87-5512.</p> <p>Location/Qualifiers</p> <ul style="list-style-type: none"> 1. .1083 1. .1083 <p>/codon_start=1 /product="Monocyte Chemoattractant Protein 1 Receptor" /protein_id="BA06253.1" /translation="MILSTSRSPRINTNESGEVTFDYDGYAPGCHFDYKQIAQL LPPLYSLVVEFGVGMVLVILINCKLCLTDIYLNAAISDULFLITLPLWAISA ANEWFGNAACKLFLTGLYHICYFGGFFLILLLTIDELYLAVHAYFALKARVTFGVTT SVTIVLAVATASVPGVLTGTFIYQKOCESVYVGGPYFPRGWNNTHTIMNLGIVLPLLIM VICYSGILKILTCRCLNEKKHRRAVRYIFTMIVYVFLWTPNIVNTTGFQFGLSN CESTPSQDQVATVLTGMMHCKCINPIIYAVGKFRRLYSVFFERKHTRECKQCPV FYTERDVGYSTNTSTGEGEVSAGI"</p>
CDS	

query Match	Score	DB	Length
best Local Similarity	39.98;	Score 890;	1083;
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220	ATGGTGGTGTGTCATCTTAATAACTGCAAAAGCTGTTACTGACATTAC	219	
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280	CTGCTCAACCTGGCCATCTCGTATCTTCTTCTTATTACCTCCCATGTGGCTAC	339	
241	CTGCTCAACCTGGCCATCTCGTATCTTCTTCTTATTACCTCCCATGTGGCTAC	339	
340	TCTGCTGCAAAAGTGAATGGGGCTTGGGAATGGGAATTATTCACAGGGCTAT	300	
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400	CACATCGTTATTTGGGGAAATCTCTCATCATCTCCGACANTCGAATGATACCTG	459	
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460	GCTATGTCATGCTGCTGTTGCTTAAACCCAGAACGGTACCGTGGTGGTGGAC	519	
421	GCTATGTCATGCTGCTGTTGCTTAAACCCAGAACGGTACCGTGGTGGTGGAC	480	
520	AGTGTGATCACCTGCTGGTGGCTGCTGTTGCTTCTGTCAGGATCATCTTAACTA	579	

Db	481	AGTGATCACCTGGTTGGGGCTGTGTTGCCATCTTTCTGTCAGGAAATCATCTTAA	540
QY	580	TGCCGAAAGAAGATTCCTTTATGTCCTGCGCCCTTATTTCACAGGATGGATAT	639
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QY	640	TTCCACACAAATAATGAGAACATTGCGCTGCTGCCCTGTCATCATGGTCATC	699
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QY	700	TGCTACTGGGAATCCTGAAACCTGCTTGGTGAAGAGAAAGGGCATAGG	759
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QY	760	GCAGTGAGCTCATCTCACCATCATGATGTTTACTTTCTCTGGACTCCCTATAAC	819
Db	721	GCAGTGAGCTCATCTCACCATCATGATGTTTACTTTCTCTGGACTCCCTATAAC	780
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QY	880	AGTCACTGGCCAAGCCACCGAGTGCACAGAGACTCTGGATGACTCTGTGCTC	939
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QY	940	AATCCCATCATCTGCTTCCTGTTGGGAGAGTCAGAG	980
Db	901	AATCCCATCATCTGCTTCCTGTTGGGAGAGTCAGAG	941

Ddb	181	ATGCGGTGCTGCTCATCTAAACTGCAAAAGCTGAAAGTGGCTGACTGACATTAC	240
Qy	280	CTGCTCAACCTGGCCATCTGATCTGCTTCTCTTCTTATTACTCTCCATCTGGCTCAC	339
Db	241	CTGCTCAACCTGGCCATCTGATCTGCTTCTCTTCTTATTACTCTCCATCTGGCTCAC	300
Qy	340	TCTGTGCAAATGATGATGGGCTCTTGGAAATGCAATSTGCAATTATTCACAGGGCTAT	399
Db	301	TCTGTGCAAATGATGATGGGCTCTTGGAAATGCAATTCACAGGGCTAT	360
Qy	400	CACATCGGTATTTCGGGAATCTCTTCATCATCTCCCTGACATCGATAGATACCTG	459
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Qy	460	GCTATATGTCATGCTGTTGCTTAAAGCCAGGACGGTCACTTGTGGGTGGTGTGACA	519
Db	421	GCTATATGTCATGCTGTTGCTTAAAGCCAGGACGGTCACTTGTGGGTGGTGTGACA	480
Qy	520	AGTGTGATCACCTGTTGTTGTGCTTGTCCAGGAACTTGTCCAGGAACTCATCTTAA	579
Db	481	AGTGTGATCACCTGTTGTTGTGCTTGTCCAGGAACTTGTCCAGGAACTCATCTTAA	540
Qy	580	TGCCAGAAAAGAGATTCCTGTTATGTCGTGCCCCATTATTCACGGAGATGGAAATAAT	639
Db	541	TGCCAGAAAAGAGATTCCTGTTATGTCGTGCCCCATTATTCACGGAGATGGAAATAAT	600
Qy	640	TTCACACAAATAATGAGAAACATTGGGCTGTGCTTCTCCGCTCATCATGGTCATC	699
Db	601	TTCACACAAATAATGAGAAACATTGGGCTGTGCTTCTCCGCTCATCATGGTCATC	666
Qy	700	TGCTACTCGGAACTCTGAAACCTGTTCTGGGTGCTGAAACGGAAAGAGGGCATAGG	755
Db	661	TGCTACTCGGAACTCTGAAACCTGTTCTGGGTGCTGAAACGGAAAGAGGGCATAGG	722
Qy	760	GCACTGAGGTCACTTCACCATATGATGTTACTTCTCTGGACTCCCTATAAAC	811
Db	721	GCACTGAGGTCACTTCACCATATGATGTTACTTCTCTGGACTCCCTATAAAC	781
Qy	820	ATTGTCATCTCCCTGAAACCTCTGGAAATTCTGGCTGATGTAACCTGTGAAAGCACC	877
Db	781	ATTGTCATCTCCCTGAAACCTCTGGAAATTCTGGCTGATGTAACCTGTGAAAGCACC	841
Qy	880	AGTCAACTGGACCAAGGCCAGGTGACAGAGACTCTGGATGACTCACTGCGCATC	93
Db	841	AGTCAACTGGACCAAGGCCAGGTGACAGAGACTCTGGATGACTCACTGCGCATC	90
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Db	901	AATCCCATCATCTAAGCCCTCTGGAGAAGTTCAAGAG	941

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